STIC-Bi	ot ch/ChemLib	84872
From:	Schnizer, Holly	フェクミルとり

Tuesday, January 21, 2003 4:44 PM STIC-Biotech/ChemLib Sent: To: Subject: seq. search for appl. no. 09/435,403

シークロストロ

JAN 22 2003

Please search the commercial and interference databases for the following

(STIC) (S19)

1) Arg Pro Asn Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile (this sequence is SEQ ID NO: 2 wherein Leu at position 3 is mutated to Asn)

Thank you.

Holly Schnizer AU 1653 CM1-9E09 305-3722 mailbox: CM/1-9B01

> Punt of Contact: Toby Port Technical Info. Specialist CUM 6A9A 703-308-3534

	TYPE OF SEARCH:
Searcher:	NA Sequences:
Phone:	AA Sequences:
Location:	Structures:
Date Picked Up: 1/23	Bibliographic:
Date Completed: 1123	Litigation:
Searcher Prep/Review:	Full text:
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VENDOR/COST (where applic.)
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7		93.4	4		AAR74090	Factor-VIII heavy
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haemophilia-A coagulant; blood; A 368 blood-clotting; peptide; 94WO-DK00424 93DK-0001281 fragment entry) AS NOVO-NORDISK (first standard; -VIII -1994 ; Human Factor Factor-VIII; sapiens WO9513301-A. -1993; -199521-NOV-1995 罚 AAR73020 AAR73020 Persson $\overline{}$ 12-NOV 18-MAY 10-NOV (NOVO Homo AAR7302
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08;
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96.0%;
/ative
                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                        94WO-DK00423
                                                                                                                                                                                                                                                                                                                                                                                93DK-0001280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kjalke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIII polypeptide(s)
                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     easier
 larity 96.
Conservative
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terminal epitope(s)
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                                                                                                                                                                                  (first
                                                                                                                                                                                                                                   VIII;
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                                                                                                                                 standard;
 Similarity
24; Conser
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n cleavage;
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24; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                            sapiens
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                                                                                                                                                                                   -1995
                                                                                                                                                                                                             Factor-VIII
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AAR76961
ID AAR7
XX
AC AAR7
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09-MAR-1996

Homo

13-JUL-1995

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comprises

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Cys

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The new Factor-VIII derivative comprises a functional A2 domain in which Cys-692 is replaced with Ser. For other (less preferred) substitutions at this site, see AAR76961. Alternatively, Glu-720 Tyr-729 are deleted or substituted with various amino acids (as in the Features). The new derivative has the same activity as the withe Factor-VIII but with improved stability (the activity is maintained for a longer period compared to the rapid decline of the activity of wt Factor-VIII). The new derivative can be used in a composition for treating diseases caused by an absence or deficient of Factor-VIII, especially haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemophilia-A
                                                                                                                                                                                                                haemophilia
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1.4e-10;
1;
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containing
                                  Ser,
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                                                     Ala
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Mismatches
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Pred. No. 4
                                  Gln,
                                                     Val,
                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   blood;
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                                   or
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96.0%;
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   692
/label=
720
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729
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                                                                                                                                                                                                                                                      18-20;
                                                                                                                                                    ) NOVO-NORDISK
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24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VIII
                                                                                                                                                                                                                                   residues
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                                                                                                                                                                         Rasmussen
   Misc-difference
                       Misc-difference
                                            erence
                                                                                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                               factor
ises a f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Factor
                                                                                                                                  -JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actor-VIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                           13-JUL-1995
                                                                                                                                                                                                                                                       Disclosure;
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Best Loc
Matches
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AAR73021
ID AAR7
XX
AC AAR7
XX
DT 21-N
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DE HUMB
XX
VX
CS HOMC
XX
PD HOMC
XX
PP 10-N
XX
PP 12-N
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PF 10-N
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PF 12-N
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PR 12-N
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PR XX
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                                                                                                                                                                                                                                                                                                                                                   is a functional A2 downs
th another amino acid
Alternatively, Glu-720 a
-inus amino acids (as i
                                                                                                                                                                                                                                                                                                                                               which Cys-692 is deleted or replaced with another amino acid residue, preferably Ser (see AAR76962). Alternatively, Glu-720 Tyr-729 are deleted or substituted with various amino acids (as the Features). The new derivative has the same activity as the type Factor-VIII but with improved stability (the activity is maintained for a longer period compared to the rapid decline of activity of wt Factor-VIII). The new derivative can be used in composition for treating diseases caused by an absence or Anti-
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r a mutation
                                                                                                   Gly
                                                                                                                      Val
                                                                                                  Ser,
                                                                                                                      Thr,
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.4e-10;
es 1;
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containing
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Smatches
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Pred. No. 4.
0; Mismatche
                                       blood-clotting
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                                                                                                                     Gln,
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                                                                            Location/Qualifiers
692
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                     derivative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 96.0%; 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                       therapeutic;
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                                                                                                            /label-
                                                                                                  /label-
                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                         -17;
                                                                                                                                                                                                                                          NOVO-NORDISK
                                                                                                     720
(first
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                                                                                                                                                                                                                                                             Rasmussen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                    VIII
                     -VIII
                                                                                                                                                                                                                                                                                                                         residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VIII
                                                                                                                                                                                                                                                                                                                                           Page
                                                                                      Misc-difference
                                                                                                          Misc-difference
                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740
                                                                                                                                                                                                                                                                                                    factor
                                                                                                                                                          WO9518827-A1
                     Factor
                                       Factor-VIII;
                                                           sapiens
                                                                                                                                                                                                06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Factor
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-VIII

Factor

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Human

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Ouery Match Best Local S Matches 24

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The fragments may k
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises
                                                                                                                                                                                                                 Human factor
                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                           WO9518828-A1
                                                                                                                                                                                                                                                                                                                                                                                06-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    -JAN-1994;
                                                                                                                                                                                                                                    VIII;
                                                                                                                                                                                                                                                                                                                                                               13-JUL-1995
                                                                                                                                                                                              21-FEB-1996
                                                                                                                                                                            AAR76982;
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                                                 Match
                              Sequence
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                                                         Local
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                                                                                                                                                                                                                                    Factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Ezban
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                                                          Best Lo
                                                                                                        484
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                                                                                                                                    RESULT 8
AAR76982
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ain coagulant
antibodies to
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents N-terminal residues 1-740 of a human Factor VIII heavy chain. The sequence contains entire A1 and A2 domains, and truncated forms (1-720 in (AAR74088) and 1-729 in (AAR74090)) may be produced by treatment with a protease, e.g. thrombin. The C-terminally truncated fragments have the same coagulant specific activity as full-length Factor-VIII, and may be produced recombinantly to reduce production costs and improve safety, giving higher production levels and stability than for the full-length form
                                                         sting
                                                                                                                             thrombin
                                     le - is prepd. usi
l suberate in the
with long lasting
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of high
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                                                                                                        of human Factor-VIII which maded stability and retention of filme after activation by the nt or treat diseases caused by VIII in a subject such as
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                                                                                                                                                                                               Length
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                                      which is stable disuccinimydyl sice a coagulant wi
                                                                                                                                                                                                16;
-10;
1
                                                                                                                                                                                              Score 127; DB 1
Pred. No. 4.4e-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               fragment
                                                                                                                                                                                                                                                                                                                                                                                 -terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s) comprising a r to produce rec treat patients Factor VIII
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                                      polypeptide wh
suberate or di
80 to produce
                                                                                                         This is the N-terminal fragment of hun crosslinked resulting in increased statetivity over extended periods of time The polypeptide is used to prevent or absence or deficiency of Factor-VIII is
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                                                                                       36pp; English
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l Similarity 96.0%;
24; Conservative
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                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : VIII polypeptide(s)
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sed to
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                                      Crosslinked Factor VIII
bis(sulphosuccinimydyl)
presence of polysorbate
activity
                                                                                                                                                                                                                                                                                                                                                               chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epitope(s)
                                                                                       Page 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NORDISK
                                                                                                                                                                                                                                                                                                                                                                                VIII;
                                                                                                                                                                                                                                                                                                                                             (first
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                     1995-194038/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rasmussen M,
                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                            cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                 heavy
                                                                                                                                                                             740
                                                                                                                                                                                                                                                                                                                                                                                  Factor
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                                                                                        Disclosure;
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Al-A2 doma
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Best Local S
Matches 24
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   Persson
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                    WPI;
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reactions. Factor VIII is an essential part of the clotting
reaction in response to a wound. Factor VIII is susceptible to cleavage
by thrombin, activated protein C. plasmin, and other serine proteases.

Eull length factor VIII consists of three repeats of the A-domain, a
Gomain and 2 repeats of the C-domain. Active factor VIII has the Al
domain cleaved off. Factor VIII is too unstable for use in recombinant
cenniques. Factor VIII containing this sequence has improved stability
and shows resistance against enzymatic activity present in mammalian
cells. This means that factor VIII derivative can be used for
treating diseases caused by an absence or deficiency of factor VIII (in
the same way as normal factor VIII) e.g. haemophilia. The advantage with
using a recombinant factor VIII) e.g. haemophilia. The advantage with
using a recombinant factor VIII also includes no need for lots of donors
to norder to get a sufficient amount. Also, there is no longer of transmirely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lia. The advantage with need for lots of donors is no long purification blood-bourne diseases
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                                                                                   Length 740;
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Glu720 and/or 1
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patients who have C-terminal part of
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therapy; deficiency.
                                                                                   Score 127; DB 16;
Pred. No. 4.4e-10;
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se; recombination;
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AHRTPMPKIQNVSSSDLLMLL is inserted
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VIII (FVIII) mutant protein, comprising a deletion of the B domain and von Willebrand factor binding site, a mutation at Arg740 and an addition of an amino acid sequence spacer between the A2 and A3 domains. Factor VIII, along with calcium and phospholipid, acts as a cofactor for factor IXA, when it converts factor X to the activated form (factor for factor is the coagultion factor deficient in the X-chromosome-linked bleeding disorder haemophilia A. Several other mutant FVIII proteins have also been created (see AAW3322-29). The FVIII mutant F309S (AAW33225) is capable of recombinant secretion at higher levels than typically obtained with wild type FVIII and retains pro-coagulant activity. The FVIII mutant R336I (AAW3322) and R562K (AAW33223) are resistant to activated protein C (APC) cleavage. The present FVIII mutant can form a more stable configuration, and have an approximate 5-fold increase in specific activity compared to purified wild type FVIII, while increasing their binding affinity to von Willebrand factor improves their stability. The FVIII proteins can be administered to haemophiliacs, i.e. for gene theorem.
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Pred. No. 8.6e-10;
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station at Arg740 and an addition of an amino acrostween the A2 and A3 domains can form a more stable have an approximate 5-fold increase in specific to purified wild type FVIII, while increasing their to von Willebrand factor improves their stability. Stan be administered to haemophiliacs, i.e. FVIII
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ant activity; resistance
B domain; A2 domain; A3
binding affinity;
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SFSQNSRHPSTROKQFNATTIPENDIEKTDPWF
AHRTPMPKIQNVSSSDLLMLL is inserted
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FVIII

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The present sequence represents a novel pro-coagulant active factor VIII (FVIII) mutant protein, comprising a deletion of the B domain and von Willebrand factor binding site, mutations F309S, R740A and addition of an amino acid sequence spacer between the A2 and A3 domains. Factor VIII, along with calcium and phospholipid, acts as a cofactor for factor IXA, when it converts factor X to the activated form (factor XA). FVIII is the coagultion factor deficient in the X-chromosome-linked bleeding disorder haemophilia A. Several other mutant FVIII proteins have also been created (see AAW3322-29). The FVIII mutant F309S (AAW3325) is capable of recombinant secretion at higher levels than typically obtained with wild type FVIII and retains pro-coagulant activity. The FVIII mutant C (APC) cleavage. The present FVIII mutant can form a more stable configuration, and have an approximate 5-fold increase in specific activity compared to purified wild type FVIII, while increasing their binding affinity to von Willebrand factor improves their stability. The FVIII proteins can be administered to haemophiliacs, i.e.
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replacement
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yield transformation
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The full lenght Factor VIII:C cDNA has two changes with respect to to published sequence (EPO application 160457):

CTG to CTA at Leu 242 and TTC to CTC change at amino acid residue 18 (Phe to Leu). The product is produced in approx. 20 times higher yields than previous recombinant produced factor VIII:C and are more easily purified. The peptide is used for treating haemophilia A, botles also AAN80444 and AAN80446.
                                                                                                                                                                                                                                       residue
s higher
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                                                                                                                                  Arg-740 of the carboxyl terminus of the H chain is directly bonded by a peptide bond to Glu-1649 of the amino terminus of L chain. A prefd. expression vector used to transform animal cell so that they produce human Factor VIII:Cis plasmid Ad.RE.neo.

The expression vector has at least one promoter upstream of AAN90654.

The transformants can constantly and continuously produce human Factor VIII:C in high yield on a commercial scale. The human Factor VIII:C so produced is considered to corresp. to the smallest species of active an intact Factor VIII:C molecules in the human blood plasma. It is useful for treating haemophilia A patients.
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(receptor-dependent) clearance of factor VIII, while C2 domain mutants have reduced receptor-independent clearance. The invention also relates to a method of using RAP (receptor associated protein), a protein which inhibits LRP (low density lipoprotein related protein) mediated ligand internalisation, to increase the half-life of factor VIII. The mutant factor VIII proteins, and nucleotides encoding them, are useful for treating haemophilia. RAP, LRP-binding RAP mutants or fragments, and nucleic acids encoding them may also be used in the treatment of haemophilia, in combination with a mutant factor VIII protein or DNA of the invention. The invention provides means of increasing the half-life of factor VIII by reducing its clearance from plasma. The present sequence represents a mutant mature human factor VIII which lacks a B
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The full lenght Factor VIII:C cDNA has two changes with respect to the published sequence (EPO application 160457):

CTG to CTA at Leu 242 and TTC to CTC change at amino acid residue 1880 (Phe to Leu). The product is produced in approx. 20 times higher yields than previous recombinant produced factor VIII:C and are more easily purified. The peptide is used for treating haemophilla A, both acute and prolonged bleeding.

See also AAN80444 and AAN80447.
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SEQ2-ASNAT3 136 1 RPnYSRRLPKGVKHLKDFPILPGEI

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Hartog, K.; Hansen, o. 32803 D.; Ha .; Dina, D. Favalaro,

VIII ctor human cogulation factor VIII precursor (validated) - human N.Alternate names: antihemophilic factor A; coagulation factor C; Species: 1900 appleas (man) (C; Species: 1900 appleas) (man) (C; Species: 100 appleas) (man) (man) (C; Species: 100 appleas) (man) (man)

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Nature 312, 326-330, 1984
A;Title: Characterization of the human facto
A;Reference number: A56196; MUID:85061547; P
A;Contents: annotation; introns
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.;
Protein Sci. 4, 740-746, 1995
A;Title: Locations of disulfide bonds and fi
A;Reference number: A56216; MUID:95338127; E
A;Contents: annotation; disulfide bonds
A;Note: 329-Cys, 711-Cys, and 2019-Cys were
R;Kjalke, M.; Heding, A.; Talbo, G.; Persson
Eur. J. Biochem. 234, 773-779, 1995
A;Title: Amino acid residues 721-729 are rec
A;Peference number: S63527; MUID:96163459; I
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d, P.; Larsson, K.; S
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C; Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_char
C; Accession: A47004
R; Elder, B.; Lakich, D.; Gitschier, J.
Genomics 16, 374-379, 1993
A; Title: Sequence of the murine factor VIII cDNA.
A; Reference number: A47004; MUID: 93300511; PMID: 8314577
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Silva, F.
Van Sluys
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JC4591
alpha-1,3 fucosyltransferase (EC 2.4.1.-)
C; Species: Mus musculus (house mouse)
C; Date: 16-Apr-1996 #sequence_revision 24
C; Accession: JC4591
R; Ozawa, M.; Muramatsu, T.
J. Biochem. 119, 302-308, 1996
A; Title: Molecular cloning and expression A; Reference number: JC4591; MUID:97037075
A; Accession: JC4591
A; Molecule type: mRNA
A; Residues: 1-400 <02A>
A; Experimental source: Embryonal carcinom C; Superfamily: galactoside 3(4)-L-fucosyl C; Keywords: glycoprotein; glycosyltransfe F; 1-23/Domain: intracellular #status pref F; 84,185/Bomain: transmembrane #status pref F; 84,185/Bomain: transmembrane #status pref F; 84,185/Bomain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                    Horíkawa,
Tanaka, T
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G71070
hypothetical protein PH1259 - Pyr.
C; Species: Pyrococcus horikoshii
C; Date: 14-Aug-1998 #sequence_rev
C; Accession: G71070
R; Kawarabayasi, Y.; Sawada, M.; Hi
M.; Ohfuku, Y.; Funahashi, T.; Ti
DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and ge
A; Title: Complete sequence and ge
A; Reference number: A71000; MUID:
A; Reference number: A71000; MUID:
A; Accession: G71070
A; Status: preliminary; nucleic ac
A; Molecule type: DNA
A; Residues: 1-412 < KAW>
A; Residues: 1-412 < KAW>
A; Cross-references: GB:AP000005;
A; Experimental source: strain OT3
A; Note: this accession replaces a
C; Genetics:
A; Gene: PH1259
C; Superfamily: hypothetical prote
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A; Authors: da Silva, A.C.R.;
M.; Tsubako, M.H.; Vallada, I
A; Reference number: A59328
A; Contents: annotation
C; Genetics:
A; Gene: XF2237
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A02583
conserved hypothetical protein XF2237 [limp.c...
C.Species: Xylella fastidiosa
C.Species: Aylella fastidiosa
C.Species: Aylella fastidiosa
C.Accession: A22583
C.Accession: A22583
C.Accession: A22583
C.Accession: A22585
Reference number: A22515; Mu10:20365717; PMID:10910347
R.Note: for a complete list of authors see reference number A59328 below
A.Steaus: preliminary
A.Note: for a complete list of authors see reference number A59328 below
A.Steaus: preliminary
A.Note: Loss references: GB:AE0003849; NID:99107384; PIDN:AAP85036.1; GSPDB:GNO1
A.Steaus: preliminary
A.Steaus: Description A.J.G.; Reinach, F.C.; Arruda, P.; Ahreu, F.A.; Acencio, M.; Alvarenga, R.; A. Robers M. R. S.; Bueno, M. R. P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, B. Briones, M. E.; Doerry, H.; Pecincani, A.D.; Frencia, A.J.G.; Reinach, P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, B. Submitted to GenBank, June 2000
A.Authors: Perreira, V.C.A.; Perro, A. M.; Marcins, E. E.; Marchal, C.Y.; Franco, C.L.; Marques, M.V.; Martins, E. A. Authors: Martins, E. M.; Macher, B. M.; Madelra, M. A.; Mad
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C; Species: Arabidopsis thaliana (Mouse-ear cress)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_chang
C; Accession: T04583; T05507
R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Esband, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Esterence number: 215378
A; Molecule type: DNA
A; Residues: 1-1607 < BEV>
A; Cross-references: EMBL:AL022141
A; Experimental source: cultivar Columbia; BAC clone F23E13
R; Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.; Submitted to the Protein Sequence Database, April 1998
A; Reference number: 215418
A; Accession: T05507
A; Molecule type: DNA
A; Residues: 1448-1607 < BE2>
A; Cross-references: EMBL:AL022373
A; Residues: 1448-1607 < BE2>
A; Cross-references: EMBL:AL022373
A; Experimental source: cultivar Columbia; BAC clone T19K4
C; Genetics:
A; Map position: 4
A; Introns: 19372; 238/2; 556/2; 930/3; 1287/3
A; Note: F23E13.30; T19K4.270
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A; Accession: A57596
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-433 <GER>
A; Residues: 1-433 <GER>
C; Superfamily: galactoside 3(4)-L-fucosyltransferase
C; Keywords: glycosyltransferase; hexosyltransferase
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T45787
disease resistance-like protein - Arabidopsis thalians
N;Alternate names: protein F26013.200
C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #to
C;Accession: T45787
R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Lay
Submitted to the Protein Sequence Database, December 3
A;Accession: T45787
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Experimental source: cultivar Columbia; BAC clone F;
C;Genetics:
A;Map position: 3
A;Introns: 138/2; 490/3; 589/3; 1047/3
A;Note: F26013.200
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Molecule type: mRNA
Rocession: A36340
Molecule type: mRNA
Residues: 'MRRLWGAARKPSGAGWEKEWAEAPQEAPGAWSGRLGPGR','SGRKGRAVPGWASWPAHLALAARPARHLGGAGG
Cross-references: GB:M58597; NID:g182070; PIDN:AAA63173.1; PID:g182071
Cross-references: GB:M58597; NID:g182070; PIDN:AAA63173.1; PID:g182071
Note: the codon used as an initiator for this translation is not in a good context for Note: the codon used as an initiator for this translation is not in a good context for Lowe, J.B.; Kukowska-Latallo, J.F.; Nair, R.P.; Larsen, R.D.; Marks, R.M.; Macher, B.P.
Elol. Chem. 266, 17467-17477, 1991
Title: Molecular cloning of a human fucosyltransferase gene that determines expression Reference number: A40976; MUID:91373370; PMID:1716630
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alpha(1,3)-fucosyltransferase (BC 2.4.1..) 4 precursor [validated] - human alpha(1,3)-fucosyltransferase (BC 2.4.1..) 4 precursor [validated] - human value (C. Species: Homo sapiens: CD15; ELM*1 ligand fucosyltransferase (ELFT): FCT3A: FUC-TIN C): Species: Homo sapiens (ELM*1) ligand (E. Species: Homo sapiens (ELM*1): Albha (ELM*1): FCT3A: FUC-TIN C): Species: Homo sapiens (ELM*1): FCT3A: FUC-TIN C): Species: Homo sapiens (ELM*1): FCT3A: FUC-TIN C): Species: Homo sapiens (ELM*1): Homo sapien
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A57596
alpha-1,3-fucosyltransferase Fuc-TIV (EC 2.4.1.-) - mou
N;Alternate names: ELAM-1 ligand fucosyltransferase hor
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #te)
C;Accession: A57596
R;Gersten, K.M.; Natsuka, S.; Trinchera, M.; Petryniak,
J. Biol. Chem. 270, 25047-25056, 1995
A;Title: Molecular cloning, expression, chromosomal asserase.
A;Reference number: A57596; MUID:96027607; PMID:755963;
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S.N.; Folger,
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B83164
conserved hypothetical protein PA3847 [imported] -
C; Species: Pseudomonas aeruginosa
C; Species: 15-Sep-2000 #sequence_revision 15-Sep-2000
C; Accession: B83164
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.: Fr
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HYALHLPKGVKSLPEELRLLHWEHFPLL
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laminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 2 - moth orchid (Species: Doritaenopsis sp. (moth orchid) (Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 04-Feb-2000 (SAccession: S54011 R;Bui, A.Q.; O'Neill, S.D. submitted to the EMBL Data Library, January 1993 A;Description: Molecular cloning and characterization of cDNAs encoding 1-aminocyclop A;Reference number: S54011 A;Reference number: S54011 A;Residues: 1-444 <BUI>A;Residues: 1-444 <BUI>A;Residues: 1-444 <BUI>A;Cross-references: EMBL:L07883; NID:g167980; FIDN:AAB05849.1; PID:g167981 C;Genetics: A;Gene: ACS2 C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase C;Reywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal pho F;272/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                       GSPDB:GN00068;
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A; Status: preliminary; tra
A; Molecule type: DNA
A; Residues: 1-1690 <HIL>
A; Cross-references: EMBL:P
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A; Gene: SPDB:SPCC1183.07
A; Map position: 3
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B46642
DNA-directed DNA polymerase (EC 2.7.7.7) alpha C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-C; Accession: B46642
R; Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R; Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R; Miblel: Chem. 268, 8111-8122, 1993
A; Title: Molecular cloning of the cDNAs for the A; Reference number: A46642; MUID:93216788; PMIA; Accession: B46642
A; Reference number: A46642; MUID:93216788; PMIA; Molecule type: mRNA; protein
A; Residues: 1-600 <MIY>
A; Molecule type: mRNA; protein
A; Experimental source: FM3A cells
A; Experimental source: FM3A cells
A; Note: sequence extracted from NCBI backbone
C; Keywords: nucleotidyltransferase
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	"Characterization of the polypeptide composition of number lactor VIII:C and the nucleotide sequence and expression of the human kidney
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analysis of amplified hemophilia DNA sequences.";
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VARIANTS PHE-1699 AND CYS-1708.
MEDLINE-90152691; PubMed-2105906;
Higuchi M., Wong C., Kochhan L., Ol
Kazazian H.H., Antonarakis S.E.;
"Characterization of mutations in t
sequencing of amplified genomic DNA
Genomics 6:65-71(1990).
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WARIANT HIS-391.

MEDLINE-89264602; PubMed-249888

Arai M., Inaba H., Higuchi M.,
Fujimaki M., Hoyer L.W.;
"Direct characterization of facmutation altering a thrombin clarginine-372-->histidine).";
Proc. Natl. Acad. Sci. U.S.A. f [21]
"Norant CYS-1708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS GLN-2228 AND LEU-2326
MEDLINE-90123183; PubMed-21051
Casula L., Murru S., Pecorara
Mancuso G., Morfini M., de Bia
"Recurrent mutations and three
VIII gene of hemophilia A pati
Blood 75:662-670(1990).
[23]
VARIANT CYS-391.
MEDLINE-90329422; PubMed-19739
Pattinson J.K., McVey J.H., Bc
"CRM+ haemophilia A due to a r
internal heavy chain thrombin
Br. J. Haematol. 75:73-77(1991
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                                                                                                                                                                                                         resulting in mc
Blood 74:2688-2691(15
[19]
VARIANT LEU-2326.
MEDLINE-89197216; Pu
Inaba H., Fujimaki M
"Mild hemophilia A r
t the factor VIII c
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"Purification nonfunctional A.";
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01-NOV-1997
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Tagenomics 16:374-379(1993).

Lefter B., Lakich D., Gitschier J.;

Genomics 16:374-379(1993).

-!- FUNCTION: FACTOR VIII, ALONG WITH CALCIUM AND PHOSPHOLIPID, ACTS

AS A COPACTOR FOR EACTOR IXA WHEN IT CONVERTS FACTOR X TO THE

ACTIVATED FORM, FACTOR XA.

-!- SUBCELLUIAR LOCATION: Extracellular.

-!- TISSUE SPECIFICITY: FOUND IN MOST TISSUES.

-!- SIMILARITY: CONTAINS 3 F5/8 TYPE A DOMAINS; EACH IS COMPOSED OF

C. -!- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

-!- SIMILARITY: STRONG, TO COAGULATION FACTOR V.

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MGD; MGI:88383; F8.
InterPro; IPR001117; Cu-oxidase.
InterPro; IPR001117; Cu-oxidase.
Pfam; PF00394; Cu-oxidase; 3.
Pfam; PF00754; F5_F8_type_C; 2.
SMART; SM00231; FA58C; 2.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
Blood coagulation; Repeat; Plasma; Acute Signal; Glycoprotein; Sulfation.
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Eukaryota; Metazoa; Chordata; Crani; Mammalia; Eutheria; Rodentia; Sciure NCBI_TaxID=10090;
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A large Gigensalue Corn vitro procedulated to 54 km) of human factor viii and dispensalue Corn vitro procedulated activity.

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PLASTOCYANIN-LIKE 6.
F5/8 TYPE C 1.
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R.J.;
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01-N05-1996 (Rel. 34, Last sequence update)
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01-N08-2002 (Rel. 34, Last sequence update)
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on modified and this statement is not removed. Usage by and for commercientiles requires a license agreement (See http://www.isb-sib.ch/announkor send an email to license@isb-sib.ch).
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LUMENAL, CATALYTIC (POTEIN N-LINKED (GLCNAC. . .) (IN PEF. 2 AND 3)
E -> D (IN REF. 3).
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Pred. No.
3; Mismat
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MEDLINE=96027607; PubMed=7559635;
Gersten K.M., Natsuka S., Trinchera M
Hiraiwa N., Jenkins N.A., Gilbert D.J
"Molecular cloning, expression, chromspecific expression of a murine alpha
corresponding to the human ELAM-1 light
Siol. Chem. 266:21777-21783(1991)
FUNCTION: MAY CATALYSE ALPHA-1,3
THE EXPRESSION OF LEWIS X/SSEA-1
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                     PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: TYPE I FORM IN TRANS CISTERNAE OF G SIMILARITY: BELONGS TO THE G
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10852; Glyco_transf=10;
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1chor; Golgi stack.
1 22 CY'
23 47 SI
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EMBL; M58596; AAA63172.1;
EMBL; M58597; AAA63173.1;
EMBL; S65161; AAB20349.1;
PIR; A36340; A36340.
Genew; HGNC:4015; FUT4.
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[2]
SEQUENCE FROM N.A.
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The observation of a mouse alpha-1,3
Thocosyltransferase gene that shows homology with the human alpha-1,3
Thocosyltransferase green that shows homology with the human alpha-1,3
Thocosyltransferase IV gene. ")
The statement of the control of a mouse alpha-1,3
Thocosyltransferase IV gene. ")
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sferase; Transmembrane; Glycc
k; Alternative splicing.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-11 ME
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LUMENAL, CATALYTIC (POTENN-LINKED (GLCNAC. .) (FOTENTIAL).

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N-LINKED (GLCNAC. .) (FOTENTIAL).

Q -> P (IN REF. 2).

R -> Q (IN REF. 2).
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15-JUL-1999 (Rel. 38
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SUBCELLULAR LOCATION: Nuclear.

PTM: PHOSPHORYLATED IN A CELL CYCLE-DEPENDENT MANNER, IN (PHASE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE DNA POLYMERASE ALPHA SUBUNIT B
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S A, B, C AND D), WHICH IS ASSEMBLED THROUGHOUT
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THE TWO SMALLEST SUBUNITS (SUBUNITS C AND D)
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              concomitant with altered physical the enzyme.";

1- FUNCTION: MAY PLAY AN ESSENTIAL ROLE AT THE CHROMOSOMAL DNA REPLICATION BY COUPLING THE ALPHA/PRIMASE COMPLEX TO THE CELLULAR REPITCATION BY COUPLING THE SIMILARITY).

1- SUBUNIT: DNA POLYMERASE ATTTT (SUBUNITS A, B, C. T.)
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                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is prod between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Use by this statement is not removed. Use that contines a license agreement (See htt or send an email to license@isb-sib.ch).
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Sciurognathi;
ropanda O., Flohr C., Thielmann H.W.;
"A mutation in the gene of subunit II of DI
Novikoff cells is concomitant with altered
properties of the enzyme.";
Submitted (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of the cDNAs for the for polymerase alpha-primase complex and their cell proliferation and the cell cycle.";
J. Biol. Chem. 268:8111-8122(1993).
-!- FUNCTION: MAY PLAY AN ESSENTIAL ROLE AT CHROMOSOMAL DNA REPLICATION BY COUPLING
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MEDLINE-93216788; PubMed-8463324;
Miyazawa H., Izumi M., Tada S., Ta
Hanaoka F.;
"Molecular cloning of the cDNAs fo
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01-FEB-1994
30-MAY-2000
DNA POLYMERA
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MEDLINE=21848401; rubmed=1180>300;

MODG V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Byouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Mooney P., Moule S., Saunders D., Seeger K., Stevens K., Stevens K., Stelton J., Simmonds M., Squares D., Seeger K., Stevens K., Stevens K., Stelton J., Simmonds M., Squares S., Stevens K., Araylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens J., Volckaert G., Aert R., Robben J., Grymonprez B., Borzym K., Langer I., Wealler H., Wambutt R., Purnelle B., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Agabet C., Moore K., Hurst S.M., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode Daga R.R., Cruzado L., Jimner M., Angal R., Angarson A., Calie L., Jimner M., Medler M., Sanchez M., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S., Benito J., Andaga R.R., Cruzado L., Jimner M., Angal L., Angal L.
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CO/SER/THR-RICH (HYDROPHILIC)

79F94BE6EF33FEBC CRC64;
PRIMASE ACTIVITY. SUBUNIT B BINDS TO SUBUNIT A. SUBCELLULAR LOCATION: Nuclear. PTM: PHOSPHORYLATED IN A CELL CYCLE-DEPENDENT MANNER,
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O13972;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine hydroxymethyltransferase, cytosolic (Serine methylase) (Glycine hydroxymethyltransferase)
SPAC24C9.12C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomyces.
NCBI_TaxID=4896;
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SEQUENCE FROM N.A.
STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
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Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";

Nature 415:871-880(2002).

-: FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.

-: CATALYTIC ACTIVITY: 5,10 methylenetetrahydrofolate + glycine +
H(2)0 = tetrahydrofolate + L-serine.

-: CATALYTIC ACTIVITY: 5,10 methylenetetrahydrofolate + glycine +
H(2)0 = tetrahydrofolate + L-serine.

-: CATALYTIC ACTIVITY: 5,10 methylenetetrahydrofolate + glycine +
H(2)0 = tetrahydrofolate + L-serine.

-: CATALYTIC ACTIVITY: FUNCATION: Cytoplasmic (BY SIMILARITY).

-: SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-: SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-: SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-: SIMILARITY: BELONGS TO THE SHMT FAMILY.

-: SIMILARITY.

-: SIMILARITY SHMT FAMILY.

-: SIMILARITY.

-: SIMILAR
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SIMPSON A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Simpson A.J.G., Reinach F.C., Arruda P., Baia G.S., Baptista C.S., A Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., A Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Boneno M.P., Colombo C., Costa M.C.R., Costa M.C.R., Costa M.C.R., Cottinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., RA Facincani A.P., Ferreira V.C.A., Ferro J.A., RA Facincani A.P., Ferreira V.C.A., Ferro J.A., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P., RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., RA Lemos E.G.M., Lemos M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
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243 243 PYRIDOXAL PHOSPHATE (BY SIMILARITY)
238 241 POLY-THR.
467 AA; 51861 MW; 0C21D7EF010C3725 CRC64;
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UBIG_XXLFA

UBIG_XXLFA

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STANDARD; PRT; 246 AA.

Q9PAM5;

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)

3-demethylubiquinone-9 3-methyltransferase (EC 2.)

dihydroxy-5-hexaprenylbenzoate methyltransferase)

methyltransferase).

UBIG OR XF2471.

Xylella fastidiosa.

Bacteria; Proteobacteria; gamma subdivision; Xanth

Xylella.

NCBI_TaxID-2371;

[1]
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P07511; 1CJ0.
Pro; IPR001085; Gly_HyMetransf
PF00464; SHMT; 1.
IE; PS00096; SHMT; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
de Silve A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
da Silveira J.F., Silvestri M.L.2., Siqueira W.J., de Souza A.B.
de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.
vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa."
"The genome sequence of the plant pathogen Xylella fastidiosa."
"The genome sequence of the plant pathogen Xylella fastidiosa."
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-
demethylubiquinone-9 - S-adenosyl-L-homocysteine + ubiquinone-1- SIMILARITY: BELONGS TO THE UBIG/COO3 FAMILY.
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D., Rode C.K.
, Goeden M.A
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P77397; P71203; P77047;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
3-(3-hydroxy-pheny1)propionate hydroxylase (EC 1...)
MHPA OR B0347.
Escherichia.
Bacteria; Proteobacteria; gamma subdivision; Enter Escherichia.
NCBI_TaxID=562;
[1]
SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
Kawamukai M.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ dat. [2]
SEQUENCE FROM N.A.
STRAIN=K12 / CS520;
Ferrandez A., Garcia J.L., Diaz E.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ dat. [3]
SEQUENCE FROM N.A.
STRAIN=K12 / W3105;
Ferrandez A., Garcia J.L., Diaz E.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ dat. [3]
SEQUENCE FROM N.A.
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Pred. No. 12;
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C Riley M., Collado-Vides J., Glasner J.D Gregor J., Davis N.W., Kirkpatrick H.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004055; AAF85269.1; -. InterPro; IPR001601; Methyltransf InterPro; IPR000051; SAM_bind. Ubiquinone biosynthesis; Transfer
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Pred. No. 30;
4; Mismatches
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STANDARD; PRT; 438
055673;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence upda:
15-JUN-2002 (Rel. 41, Last annotation up:
UDP-N-acetylglucosamine 1-carboxyvinyltr;
(Enoylpyruvate transferase) (UDP-N-acety:
transferase) (EPT).
MURA OR MURZ OR SLR0017.
Synechocystis sp. (strain PCC 6803).
Bacteria: Cyanobacteria; Chroococcales; (NCBI_TaxID=1148;
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Kotani H.
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MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Ko
Sugiura M., Tabata S.;
"Sequence analysis of the genome
"Sequence sp. strain PCC6803.
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PCC6803.
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EMBL; D64000; BAA10199.1; -.

EMBL; D64000; BAA10199.1; -.

HSSP; P33038; 1DLG.

InterPro; IPR001986; EPSP_syntase.

ProDom; PF00275; EPSP_syntase; 1.
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egion from map positions 64% to 92% of the genome.";

NA Res. 2:153-166(1995).

- FUNCTION: CELL WALL FORMATION. ADDS ENOLPYRUVYL TO ACETYLGLUCOSAMINE (BY SIMILARITY).

- CATALYTIC ACTIVITY: Phosphoenolpyruvate + UDP-N-aceglucosamine = phosphate + UDP-N-acetyl-3-0-(1-carboglucosamine.)

- PATHWAY: Peptidoglycan biosynthesis; first step.

- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY. MU
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la; Pipoidea;
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Mesobatrachia;
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MEDLINE=96379747; PubMed=8787760;
Ramos J.W., Whittaker C.A., Desimone D.V.

"Integrin-dependent adhesive activity is inductive signals at gastrulation.";
Development 122:2873-2883(1996).

[2]
SEQUENCE OF 308-379 FROM N.A.

MEDLINE=94008528; PubMed=8404528;
Thittaker C.A., Desimone D.W.;
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ProDom; PD001867; EPSP_syntase; 1.
TIGREAMS; TIGR01072; murA; 1.
Peptidoglycan synthesis; Cell wall; Complete proteome.
ACT_SITE 129 129 BIND.
SEQUENCE 438 AA: AFC.
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INTEGRIN ALPHA-4.
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CYTOPLASMIC (POTENTIAL).
FG-GAP 1.
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FG-GAP 3.
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between the Swiss Institute of Bioinformatics a the European Bioinformatics Institute. There are use by non-profit institutions as long as its modified and this statement is not removed. Usage entities requires a license agreement (See http:/or send an email to license@isb-sib.ch).

EMBL; U54497; AAA98673.1; -.

EMBL; U10188; AAA16248.1; -.

EMBL; U5088; AAA16248.1; -.

EMBL; U5088; AAA16248.1; -.

EMBL; U10188; AAA16248.1; -.

EMBL; U5497; AAA98673.1; -.

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1- SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

1- SUBCELLULAR LOCATION: CELL SURFACE (FOTENTIAL).

1- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN: ALPHA CHAINS OF TYPE IV THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 7S DOMAIN.

1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

1- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
THESE, LOCATED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF
THESE, LOCATED IN THE NCI DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
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     Euteleostomi
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7S DOMAIN.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
OR 1558 (BY SIMILARITY).
OR 1558 (BY SIMILARITY).
BY SIMILARITY.
OR 1671 (BY SIMILARITY).
OR 1674 (BY SIMILARITY).
OR 1674 (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
MW; 65E4EA282D3D37BD CRC64;
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n; Collagen;
                                    HOMO
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6(IV),
a Xq22,
  Vertebrata; Hominidae;
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Catarrhini;
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cremew. HGNC:2208; COL4A6.

MIN; 303631;

A InterPro; IPR001087; Collagen.

R InterPro; IPR001442; ProcollagnC4.

DR Pfam; PF01391; Collagen; 23.

ProDom; PD003923; ProcollagnC4, 2.

DR SWART; SM00111; C4; 2.

KW Extracellular matrix; Connective tis KW Extracellular matrix; Connective tis KW Extracellular matrix; Connective tis FT CHAIN 16 1678 COLLA FT DOMAIN 16 1678 COLLA TRIF

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IV
                                                       NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Eye, and Kidney;
MEDLINE=94171779; PubMed=8125972;
Ochashi T., Sugimoto M., Mattei M.-G
"Identification of a new collagen IV
isolation and assignment of the gene
same locus for COL4A5.";
J. Biol. Chem. 269:7520-7526(1994).
-:- FUNCTION: TYPE IV COLLAGEN IS TH
GLOMERULAR BASEMENT MEMBRANES (G
MESHWORK TOGETHER WITH LAMININS,
Chordata;
Primates;
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MEDLINE-95014445; PubMed-7523402;
Leinonen A., Mariyama M., Mochizuki T., Tryggvason K., Reeders S "Complete primary structure of the human type IV collagen alpha chain. Comparison with structure and expression of the other alp (IV) chains.";
(IV) chains.";
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MEDLINE=97338662; PubMed=9195222;

Lemmink H.H., Schroeder C.H., Monnens L.A.H., Smeets

"The clinical spectrum of type IV collagen mutations
Hum. Mutat. 9:477-499(1997).
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MEDLINE-93054733; PubMed-1429714;
Kamagata Y., Mattel M.-G., Ninomiya Y.;
"Isolation and sequencing of cDNAs and genomic DNAs alpha 4 chain of basement membrane collagen type IV the gene to the distal long arm of human chromosome J. Biol. Chem. 267:23753-23758(1992).
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MEDLINE-95078927; PubMed-7987396;

Mochizuki T., Lemmink H.H., Mariyama M
Pirson Y., Verellen-Dumoulin C., Chan I
Smeets H.J.M., Reeders S.T.;

"Identification of mutations in the all
collagen genes in autosomal recessive;
Nat. Genet. 8:77-82(1994).
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MEDLINE=98196854; PubMed=9537506;

Momota R., Sugimoto M., Ochashi T.,

Ninomiya Y.;

"Two genes, COL4A3 and COL4A4 codin
alpha4(IV) collagen chains are arra
2q36.";

FEBS Lett. 424:11-16(1998).
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FEBS Lett. 330:122-128(1993)
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=95024047; PubMed=7937893;
Wakasugi T., Tsudzuki J., Ito S., Naka
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"Loss of all ndh genes as determined k
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Proc. Natl. Acad. Sci. U.S.A. 91:9794-
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O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Putative disease resistance protein.

F23E13.30 OR 19K4.270 OR AT4G36140.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; core eudicotylexis II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ dai
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SEQUENCE OF 1448-1607 FROM N.A.
Bevan M., Wedler H., Wambutt R., Hoheisel J., Jee
Vos P., Mewes H.W., Mayer K., Schueller C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ dai
[3]
SEQUENCE OF 1421-1607 FROM N.A.
Wedler H., Wambutt R., Mewes H.W., Lemcke K., Mayer E., Brandt A., Dues'
Wedler H., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ dai
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EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ dai
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SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ dai
EMBL; AL022141; CAA18120.1; -.
EMBL; AL022373; CAA18508.1; -.
EMBL; AL022373; CAA18508.1; -.
InterPro; IPR000167; Disease_resist.
InterPro; IPR000167; TIR_domain.
Pfam; PF00560; LRR; 3.
Pfam; PF00581; NB-ARC; 2.
Pfam; PF00581; TIR; 2.
PRINTS; PR00364; DISEASERSIST.
SMART; SM00255; TIR; 2.
SEQUENCE 1607 AA: 182785 MW; 4F8F572EC72074F
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

A Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

A Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

A Abril J.F., Agbayani A., An H.-I., Andrews-Pfannkoch C., Baldwin D.,

A Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

A Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

Beckova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

A Dordson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn W.,

A Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,

A Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

A Fosler C., Gabrielian A.E., Garn P. Hansel
 G 3₹
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng I.,
Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund C., Chen M., Kim ...
Saski C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
"Rice Genomic Sequence.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AC098566; AAL77114.1; -..
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O1-JUN-2002 (TrEMBLrel, 21, Created)
O1-JUN-2002 (TrEMBLrel, 21, Last sequence upda O1-JUN-2002 (TrEMBLrel, 21, Last annotation up Putative wall-associated protein kinase, OSJNBA0051J07.1.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryo Spermatophyta; Magnoliophyta; Liliopsida; Poal Ehrhartoideae; Oryza.
NCBI_TaxID=4530;
 Score 50; DB 1
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Pred. No. 48;
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 William William Ye J., I., Zheng X.H., Zheng X.H., Zheng Gibbs R.A., Myers E... "The genome sequence of Dicascience 287:2185-2195(2000).

EMBL; AE003721; AAF55548.1; -... "IvBase; FBgn0038611; CG14309." "IvBase; FBgn0038611; CG14309." "The gase AA; 106883 MW; ARF SAA; 106883 MW; Pre
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 similarity 47.6%;
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 SEQUENCE FROM N.A.
Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Ninomiya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irle R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AKO56514; BAB71201.1: -.
SEQUENCE 579 AA, 65949 MW; 195AEFB2F4235C84 CRC64;
 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN~CV. NIPPONBARE;
MCCOmbie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,
Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSJNBa0011A24, from chromosome 10, complete sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC113336; AAM01181.1; -.
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 Tracheophyta
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 01-JUN-2002 (TrEMBLrel. 21, Created)
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5 Putative wall-associated protein kinase.
05JNBA0011A24.33.
0ryza sativa (japonica cultivar-group).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheop.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBI_TaxID=39947;
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ31952 fis, clone NT2RP7007221, weakly similar
norvegicus schlafen-4 (SLFN-4) mRNA.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Eu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; F
 Length
 Score 50; DB 10;
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 sh 36.8%;
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MEDLINE-20365717; Pubmed-10910347;

MEDLINE-20365717; Pubmed-10910347;

MEDLINE-20365717; Pubmed-10910347;

MEDLINE-20365717; Pubmed-10910347;

A alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

A buenow M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

Colautro N.B., Colombo C., Costa F.F., Costa M.C.R., Ferrer H.,

RA Facincani A.P., Perrelara A.J.S., Ferrelara V.C.A., Ferrer H.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Colombo C., Costa F.F., Costa M.C.R., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

RA HO P.L., Hobeisel J.D., Junqueira M.H.S., Gomes S.L., Gruber A.,

RA HO P.L., Hobeisel J.D., Junqueira M.H.S., Gomes S.L., Gruber A.,

RA Machado M.A., Madeira A.M.B.N., Madelia M.R., Matsuluma A.Y.,

RA Machado M.A., Madeira A.M.B.N., Matsuluma A.Y.,

RA Month A. Jr., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,

RA Molari A. Jr., Nobrega F.G., Niyaki C.Y., Monteira M.A.,

RA Golliveira M.C., de Oliveira R.C., Palmieri D.K., Paris A.,

RA de Oliveira M.C., de Oliveira R.C., Palmieri D.K., Paris A.,

RA de Rosa V.E., Tr., da Silva F.R., Silva W.A.,

RA de Silva A.M. da Silva F.R., Silva W.A.,

RA de Solva A.P., Terenil M.E., Teruli B.M., Taal S.M., Taulada H.M.,

RA de Solva A.P., Terenil M.E., Teruli B.M., Taul S.M., Taulada H.M.,

RA de Solva A.P., Terenil M.E., Teruli B.M., Taulada H.M.,

RA de Solva A.P., Terenil M.E., Teruli B.M., Taulada H.M., Taulada H.M., Van Sluys M.A., Variovski-Almeida S., Vettore A.L.,

RA de Solva A.P., Terenil M.E., Setubal J.C.;

RA Ago M.A., Zatz M., Meidanis J., Setubal J.C.;

RA Ago M.A., Zatz M., Meidanis J., Setubal J.C.;

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 melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
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 gamma subdivision; Xanthomonas group
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 ago M.A., Zatz M., Meidanis J., Setubal J.C.;
The genome sequence of the plant pathogen Xylella fast
lature 406:151-159(2000).
MBL; AE004036; AAF85036.1; -.
IYPOTHETICAL protein; Complete proteome.
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 ore 50; DB 16;
ed. No. 59;
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 ol-MAY-2000 (TrEMBLrel. 13, Created)
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Putative PAP protein (CG9936 protein).
PAP OR CG9936.
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 Score 50;
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 PubMed-10731132;
ker S.E., Holt R.A., E
Scherer S.E., Li P.W.,
01-OCT-2000 (TrEMBLrel. 15, Last s
01-MAR-2002 (TrEMBLrel. 20, Last a
Hypothetical protein Xf2237.
XF2237,
Xylella fastidiosa.
Bacteria; Proteobacteria; gamma su
Xylella.
NCBI_TaxID-2371;
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 melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
a; Drosophilidae; Drosophila.
 Boube M., Faucher C., Joulia L., Cribbs D.L., Bourbon H.M.; "The Drosophila Mediator proteins DTRAP240 and DTRAP80 are transcriptional cofactors of the proboscipedia and Sex combs Reduced homeotic proteins."; Submitted (JAN-2000) to the EMBL/Genmant/minimal Cofactors of the Cofactors
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 Baldwin D.,
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 Length 2444;
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 Length 2618;
 Treisman J.E.;

"Drosophila homologs of the transcriptional coactivation subunits TRAP240 and TRAP230 are required for identical peye-antennal disc development.";

EMBL; AF227215; AAF43172.1; -.

EMBL; AF227214; AAF43172.1; -.

EMBL; AF227214; AAF43021.1; -.

EMBL; AF227214; AAF43021.1; -.

EMBL; AF227214; AAF43021.1; -.

EMBL; AF324425; AAG48327.1; -.

FlyBase; FBgn0024200; pap.

FlyBase; FBgn0024200; pap.
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 SEQUENCE FROM N.A.
Boube M., Faucher C., Joulia L., Cribbs D.L., Bourbon Haboube M., Faucher C., Joulia L., Cribbs D.L., Bourbon Harber Drosophila Mediator proteins DTRAP240 and DTRAP80 transcriptional cofactors of the proboscipedia and Sex homeotic proteins.";
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 Hayashizaki Y.;
"Functional annotation of
Nature 409:685-690(2001).
EMBL; AK015457; BAB29855.1
MGD; MGI:1921905; 4930455
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Q1-JUN-2001 (TrEMBLre)
Q930455B06Rik protein
A930455B06Rik.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Ro
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Murinae; Mus
 Mus musculus (Mouse).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutheleostom
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN-BLG2/MSF;
Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou
"Conspicuous Differences among Gene Genealogies of 21 Nuclear G
Five Mus musculus subspecies.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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 Thermococci; Thermococcales;
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 O920V9 PRELIMINARY; PRT; 386 AA.
O920V9;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha 1,3-fucosyltransferase (Fragment).
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 17;
 Score 49; DB 11;
Pred. No. 16;
3; Mismatches
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Last sequence up
Last annotation
 Score 49; DB : Pred. No. 33; 2; Mismatches
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 058994 PRELIMINARY;
058994;
01-AUG-1998 (TrEMBLrel. 07, C
01-AUG-1998 (TrEMBLrel. 07, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein PH1259.
24508 MW;
 36.0%;
58.8%;
 Similarity 52.9%;
9; Conservative
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 NYSRRLPKGVKHLKDFP 19
 PNYSRRLPKGVKHLKDF 18
 Pyrococcus horikoshii.
Archaea; Euryarchaeota; I
Pyrococcus.
NCBI_TaxID=53953;
 Similarity 58.8
10; Conservative
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 6E057C1A29F99A70 CRC64;
 DB 11;
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 Score 48.5; D
Pred. No. 37;
3; Mismatches
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EMBL; AB039126; BAB68650.1; -.
InterPro; IPR001503; GT_10.
Pfam; PF00852; Glyco_transf_10;
Glycosyltransferase; Transferase
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43812 MW;
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 RPNYSRRLPKGV-KHLKDFP 19
 th 35.7%;
Similarity 50.0%;
10; Conservative
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 Search completed: January
Job time : 33 secs
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US-08-683-839B-3
US-08-882-083-2
US-08-858-107-2
US-08-558-107-2
US-08-212-133A-2
US-08-276-594A-2
US-08-276-594A-2
US-08-276-594A-2
US-08-276-594A-2
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US-09-324-867-3
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US-08-121-202-2
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US-09-324-867-4
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|-------------------------------------|------------------|------------------|------------------|------------------|----------|-------------------|--------------|-----------------|-----------------|-----------------|------------------|------------------|-------------------|------------------|------------------|------------------|
| US-09-315-179-6<br>US-09-523-656-28 | PCT-US94-13200-6 | US-07-864-004B-2 | US-08-251-937A-2 | PCT-US93-03275-2 | 1        | US-08-474-503-4   | -670-70      | US-09-037-601-4 | US-09-315-179-4 | US-09-523-656-4 | PCT-US94-13200-4 | US-08-121-202-4  | US-08-670-707A-39 | US-09-037-601-39 | US-09-315-179-39 | US-09-523-656-38 |
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| 94<br>94                            | 94               | 75               | 75               | 75               | 75       | 75                | 75           | 75              | 75              | 75              | 75               | 75               | 75                | 75               | 75               | 7.5              |
| 28<br>29                            | 30               | 31               | 32               | 33               | 34       | 35                | 36           | 37              | 38              | 39              | 40               | 4.4              | 42                | 43               | 44               | 45               |

ALIGNMENTS

## from Derived 1438 Length Sequence: **IIIA** 4; Factor of Artificial . рв Зе. Score 127; DB Pred. No. 3.3e 0; Mismatches for 916 US-09-209-916-1 ; Sequence 1, Application US/09209916 ; Patent No. 6358703 ; GENERAL INFORMATION: ; APPLICANT: Cho, Myung-Sam ; APPLICANT: Chan, Sham-Yuen ; APPLICANT: Kelsey, William ; APPLICANT: Yee, Helena ; TITLE OF INVENTION: Expression System fo ; FILE REFERENCE: MSB-7255 ; CURRENT APPLICATION NUMBER: US/09/209,91 ; CURRENT FILING DATE: 1998-12-10 ; NUMBER OF SEQ ID NOS: 2 ; SOFTWARE: Patentin Ver. 2.0 Description human factor Sequence .... 93.48 96.08 TYPE: PRT ORGANISM: Artificial & FEATURE: | Similarity 24; Conserv OTHER INFORMATION: 9-209-916-1 1 1438 Query Match Best Local õ 1D RESULT US-09-2 -60-

Sites

RESULT 2
US-08-683-839B-3
; Sequence 3, Application US/08683839B
; Patent No. 5744326
; GENERAL INFORMATION:
; TITLE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional
; TITLE OF INVENTION: Regulatory Sequences To Increase Expression of
; TITLE OF INVENTION: Intronless Genes Containing Near-Consensus Splice
; TITLE OF SEQUENCES: 18
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:

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HYBRID PROTEINS WITH MODIFIED ACTIVITY
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Pred. No. 3.4e-11
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JLE FORm.
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 Version
 500
 AFFLICATION NUMBER: US/08/683,839B
FILING DATE: 11-MARCH-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: """
TELECOMMUNICATION
 127;
 NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30472/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
 Suite
 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,083
 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/558,107
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
 527
 25
 us/0888208
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1471 amino acids
 ö
 SOFTWARE: Patentin Release CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/6
 Lardner
set, N.W.
 93.4%;
96.0%;
 Foley & Laru
100 K Street,
 Patent No. 5869292
GENERAL INFORMATION:
APPLICANT: VOORBERG, Joh
TITLE OF INVENTION: HYBI
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
 TELEX: 904130
INFORMATION FOR SEQ ID NO:
 Similarity 96. 24; Conservative
 protein
 SULT 3
1-08-882-083-2
Sequence 2, Application
Patent No. 5869292
 ADDRESSEE: Foley
STREET: 3000 K St
CITY: Washington
 IBM PC
SYSTEM:
 TYPE: amino acid
TOPOLOGY: linear
LECULE TYPE: pro
 READABLE
TYPE: F1
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LELEFAX: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 amino acideropology: 1:
MOLECULE TERMINATION acideropology: 1:
MO
 Score 127;
Pred. No.
 COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,107
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
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e 2, Application US/08558107
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Similarity 96.0%;
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 Sequence 2, Application Us
Patent No. 5910481
GENERAL INFORMATION:
APPLICANT: VOORBERG, J
TITLE OF INVENTION: HY
NUMBER OF SEQUENCES:
 TITLE OF INVENTION: H
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
 l amino
acid
 VOORBERG,
 ADDRESSEE: Foley STREET: 3000 K St. CITY: Washington STATE: D.C.
 Sequence 2, Application Patent No. 6130203
GENERAL INFORMATION:
APPLICANT: VOORBER
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LENGTH: AV.
TYPE: amino (TOPOLOGY: 11)
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Human/Porcine
 APPLICATION DATA:
APPLICATION NUMBER: US/09/243,539
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US 08/558,107
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30472/212
TELECOMMUNICATION INFORMATION:
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
 7/864,004B
32
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
 Suite
 COUNTRY: US
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,004:
FILING DATE: 07 APRIL 1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU106
TELECOMMUNICATION INFORMATION:
 'A:
US/09/243,539
 Sequence 4, Application US/07864004B; Patent No. 5364771; GENERAL INFORMATION:
APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Pinumber OF SEQUENCES: 6
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 RPNYSRRLPKGVKHLKDFPILPGEI
 FORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1661 amino acids
TYPE: amino acid
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Local Similarity 96.0%;
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 ONDENCE ADDRESS:
SSEE: Kilpatrick &
P: 1100 Peachtree &
Atlanta
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 TOPOLOGY: li
MOLECULE TYPE:
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 CORRESPONDENCE
ADDRESSEE:
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Human/Porcine
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/251,937A
FILING DATE: 31-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
 NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
REFERENCE/DOCKET NUMBER: EMU106DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6367
TELEFAX: 404-815-6555
 JS-US-ZZI-ZZ/A-4
; Sequence 4, Application US/08251937A
; Sequence 4, Application US/08251937A
; Patent No. 5583209
; GENERAL INFORMATION:
 APPLICANT: Lollar, John S.
; APPLICANT: Runge, Marschall S.
; TITLE OF INVENTION: Hybrid Human/Pi
; NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street
CITY: Atlanta
STATE: Georgia
; COUNTRY: US
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 ZIP: 30302
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
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OR SEQ ID NO: 4
 SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acid
TYPE: amino acid
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 EQ ID NO:
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 TOPOLOGY: 11
MOLECULE TYPE:
HYPOTHETICAL:
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TELEFAX: 40.
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:, Marschall S.
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Pred. No. 5.7e-11;
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 Score 127; DB 1;
Pred. No. 5.7e-11
); Mismatches
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 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU/76677
TELECOMMUNICATION INFORMATION:
TELEFAX: 404-572-6508
TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
 Sir.

COUNTRY: C.

ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

AMPUTER: IBM PC compatible

AMPUTER: IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

+Tn Release #1.0, VA
 APPLICATION NUMBER: US/08/212,13
FILING DATE: March 11, 1994
CLASSIFICATION: 435
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YES
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24; Conservativ
 single
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 acid
 TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
 HOMO
 ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
 MOLECULE TYPE: HYPOTHETICAL:
TYPE:
 TYPE:
 TELEFAX:
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US-08-251-937A-4
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 Score 127;
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 ALLING DATE: 24-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 243262/1991
FILING DATE: 24-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 74129/195/AOF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEO TELENGER CHAPT
 Human/Animal
 Suite
 Suite
Sequence 2, Application US/08276594A
Patent No. 5693499
GENERAL INFORMATION:
APPLICANT: YONEMURA, Hiroshi
APPLICANT: TAJIMA, Yoshitaka
APPLICANT: TAJIMA, Keishin
TITLE OF INVENTION: PROCESS FOR PRI
TITLE OF INVENTION: FACTOR VIII PROCESS FOR SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Sui
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
 508
 . Cody
Street,
 CORRESPOND.

ADDRESSEE: Foley ...
STREET: 3000 K Street, N.W., ...
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
AMEDIUM TYPE: Floppy disk
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/950
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 US/08474
 University
N: Hybrid F
ES: 12
 93.4%;
ilarity 96.0%;
Conservative
 ď.
 ADDRESSEE: Kilpatrick
STREET: 1100 Peachtree
CITY: Atlanta
 APPLICANT: Emory Unive
TITLE OF INVENTION: HY
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 SULT 10
3-08-474-503-2
Sequence 2, Application U
sequence 2, Application U
No. 574446
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 Sequence 2, Application Patent No. 5744446 GENERAL INFORMATION:
 Similarity
24; Conser
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 TYPE:
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 ATTORNEY/AGENT INFORMATION:

NAME: Pratt, John S.

REGISTRATION NUMBER: 29,476

REFERENCE/DOCKET NUMBER: EMU106CIP(3)

TELEPHONE: 404-815-6500

TELEFAX: 404-815-6555

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2332 amino acids
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 Human/Animal
 MBER: WO PCT/US94/13200
15-NOV-1994
 Score 127;
Pred. No. 5
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 TUMBER: US/08/670,707A 26-JUN-1996
 ...ek: US/08/474,503
07-JUN-1995
N: 435
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 SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
 Release
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
 Hybrid
40
 93.4%;
96.0%;
 no sapien
Liver cDNA
 ADDRESSEE: Greenlee, Win
STREET: 5370 Manhattan C
CITY: Boulder
STATE: Colorado
COUNTRY: USA
 N-terminal
 Sequence 2, Application us, of Patent No. 5859204
GENERAL INFORMATION:
APPLICANT: Lollar, John
TITLE OF INVENTION: Hybr
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
 John
 Similarity 96.
 CURRENT APPLICATION DATA
APPLICATION NUMBER: U:
FILING DATE: 07-JUN-1
CLASSIFICATION: 435
 protein
YES
 FORM:
 FILING DATE: 26-JUN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM MEDIUM TYPE: Floppy COMPUTER: IBM PC CO
 SYSTEM: P
Patentin
 Ce 2, Application Uno. 5859204
 APPLICATION NUMBER:
FILING DATE: 15-NO
 OPERATING SYSTEM:
 Homo
 IBM
 ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
 TOPOLOGY: li
MOLECULE TYPE:
HYPOTHETICAL:
 ORGANISM: HO
TISSUE TYPE:
S-08-474-503-2
 MEDIUM TYPE:
COMPUTER: I
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SOFTWARE: P
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 Human/Animal Factor VIII
 #1.30
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 DB 5.7e-
 d Sullivan,
Suite 201
 Version
 Mismatches
 FILING DATE: 26-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/13200
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA:
 Score 127;
Pred. No. 5
 APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
 ION DATA:
MBER: US/09/037,60
26-JUN-1996
 APPLICATION NUMBER: US 08/212,13
FILING DATE: 11-MAR-1994
IOR APPLICATION DATA:
 #1.0,
 and
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,6
 -95F
 -95F
 508
 25
 Winner an
an Circle
 2, Application US/09037601
. 6180371
NAME: Greenlee, Lorance L.
REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
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39,878
 REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
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TELEFAX: 303/499-8089
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 Hybrid 1
 Š
 93.4%;
96.0%;
 ... single
not relevant
E: protein
: YES
 N-terminal
 NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Wi
STREET: 5370 Manhattan
 N FOR SEO ID NO:
CHARACTERISTICS:
2332 amino aci
 Homo sapiens
 John
 Donna M
 Conservative
 FORM:
 2332 amino a STRANDEDNESS: Sirrande SURANDEDNESS: Sirrande SURANTESS: Sirrande SURFERS
 NAME: Ferber, Donn,
REGISTRATION NUMBER
REFERENCE/DOCKET NU
 RESULT 12
US-09-037-601-2
; Sequence 2, Application
; Patent No. 6180371
; GENERAL INFORMATION:
; APPLICANT: Lollar, Control of INVENTION:
 Similarity
24; Conserv
 Colorado
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TYPE: Fl
 ; ANTI-SENSE: NO
; FRAGMENT TYPE: N
; ORIGINAL SOURCE:
; ORGANISM: HOMO
; TISSUE TYPE: L
US-08-670-707A-2
 Boulder
 USA
 TOPOLOGY: not
MOLECULE TYPE:
HYPOTHETICAL: N
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 Score 127; DB 4;
Pred. No. 5.7e-11
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 RESULT 13
US-09-324-867-3
Sequence 3, Application US/09324867A
Patent No. 6251632
GENERAL INFORMATION:
APPLICANT: Lillicrap, David
APPLICANT: Cameron, Cherie
APPLICANT: No. 6251632ley, Colleen
APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene,
FILE REFERENCE: 1669.0010002/JAG/BJD
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER FILING DATE: 1998-03-05
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SOFTWARE: Patentin Ver. 2.0
 Sequence 2, Application US/09315179

Sequence 2, Application US/09315179

Patent No. 6376463

GENERAL INFORMATION:
APPLICANT: Lollar, John S

TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95H

CURRENT FILING DATE: 1999-05-20

EARLIER FILING DATE: 1999-05-20

EARLIER FILING DATE: 1998-03-10

EARLIER FILING DATE: 1996-06-26

EARLIER FILING DATE: 1996-06-26

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EARLIER FILING DATE: 1997-06-26

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EARLIER FILING DATE: 1997-06-26
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 RPNYSRRLPKGVKHLKDFPILPGEI
 93.4%;
ilarity 96.0%;
Conservative
 93.4%;
96.0%;
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Liver
 N-terminal
 Similarity 96.
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 RESULT 14
US-09-315-179-2
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Matches 24
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 ORGANISM:
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 LENGTH:
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 Score 127; DB 4;
Pred. No. 5.7e-11
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 Score 127; DB 4;
Pred. No. 5.7e-11
); Mismatches
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US-09-523-656-2
; Sequence 2, Application US/09523656
; Patent No. 6458563
; GENERAL INFORMATION:
 APPLICANT: Lollar S., John
 TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: 75-951
CURRENT APPLICATION NUMBER: US/09/523,656
; CURRENT FILING DATE: 2000-03-10
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; EARLIER FILING DATE: 1998-03-10
; EARLIER FILING DATE: 1996-06-26
; NUMBER OF SEQ ID NOS: 38
. SOFTWARE: PatentIn Ver, 2.0
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EARLIER FILING DATE: 1994-11-15
EARLIER APPLICATION NUMBER: U.S.
EARLIER FILING DATE: 1994-03-11
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EARLIER FILING DATE: 1992-04-07
NUMBER OF SEQ ID NOS: 40
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Similarity 96.0%;
24; Conservative
 Similarity 96.0
 23,
 ORGANISM: Homo sapiens -09-315-179-2
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US-09-523-656-2
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NUMBER OF SEL
SOFTWARE: Patel
SEQ ID NO 2
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ID NO 2
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SEQ2-ASNAT3 136 1 RPnYSRRLPK score Title: Perfect

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Post-processing

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## SUMMARIES

| Description   | equence 1, App | , App           | 2, App     | Sequence 2, Appli | e 4, Appl    | 49, Ap          | 8, App | 7, Appl | 11, App | 658         | e 2, | 4005, 🏚     | Sequence 2, Appli | 21   | 40, App  | 3, Appl | $1210\overline{4}$ | 438,     | Sequence 14043, A |
|---------------|----------------|-----------------|------------|-------------------|--------------|-----------------|--------|---------|---------|-------------|------|-------------|-------------------|------|----------|---------|--------------------|----------|-------------------|
| D             | US-10-006-091  | US-10-047-257-1 | us-10-095- | US-09-957-641-2   | US-10-095-71 | US-09-949-192-4 |        |         | ₽       | us-09-738-6 |      | US-09-738-6 |                   |      | 52-60-SN | -60-SN  | US-09-81           | US-09-81 | ns-0              |
| th DB         | 38             | 38 1            | 71 1       | 32 9              | 31 1         | 97 1            | 05 1   | 32 1    | 33 9    | 45 9        | 76 1 | 41 9        | 82 1              | 82 1 | 82 1     | 91 1    | 42 J               | 42 1     | 80 1              |
| y<br>sh Lengt | H              | -               | 1          | CI                | Ц            |                 |        |         |         |             |      | 7 4         |                   |      |          |         |                    | 7        | 7                 |
|               | 93.            | 93.             | 93.        | 93.               | 74.          | 36.             | 35.    | 35.     | 35.     | 34.         | 32.  | 32.         | 32.               | 32.  | 32.      | 32.     | 31.                | 31.      | 31.               |
| Score         | -              | CA              | $^{\circ}$ |                   | 0            |                 | ъ<br>В |         | ф       | 4           |      | 4           |                   |      |          |         |                    | 42.5     | ġ                 |
| Result<br>No. | <br>           | 7               | m          | 4                 | Ŋ            | 9               | 7      | ထ       | σ       |             |      | 12          |                   |      |          |         |                    |          |                   |

| Sequence 12913, A Sequence 12913, A Sequence 40747, A Sequence 43, Appl Sequence 12, Appl Sequence 259, App Sequence 14, Appl Sequence 11, Appl Sequence 11, Appl Sequence 134, Appl Sequence 134, Appl Sequence 134, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 36, Appl Sequence 35, Appl Sequence 335, Appl Sequence 6447, Appl Sequence 6447, Appl Sequence 6447, Appl Sequence 10459, Appl Seque                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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| US-09-815-242-5815<br>US-09-815-242-12913<br>US-09-864-761-40747<br>US-09-949-192-43<br>US-09-949-192-43<br>US-09-984-245-259<br>US-09-984-245-259<br>US-09-964-761-46749<br>US-09-964-761-46749<br>US-09-964-761-46749<br>US-09-964-761-46749<br>US-09-945-301-11<br>US-09-945-301-11<br>US-09-945-301-11<br>US-09-945-321-11<br>US-09-984-245-134<br>US-09-984-245-134<br>US-09-984-245-134<br>US-09-984-245-134<br>US-09-982-239-49<br>US-09-452-239-38<br>US-09-452-239-36<br>US-09-452-239-42<br>US-09-738-626-6447<br>US-09-764-860-335<br>US-09-764-860-335                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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## ALIGNMENTS

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 Length
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 VIII
 Factor
 Score 127; DB 12
Pred. No. 2.8e-11
); Mismatches
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 of Artificial vIII sequence
RESULT 1

US-10-006-091-1

Sequence 1, Application US/10006091

Patent No. US20020102730A1

GENERAL INFORMATION:

APPLICANT: Chan, Sham-Yuen

APPLICANT: Chan, Sham-Yuen

APPLICANT: Kelsey, William

APPLICANT: Yee, Helena

TITLE OF INVENTION: Expression System for Faction Reference:

CURRENT APPLICATION NUMBER: US/10/006,091

CURRENT FILING DATE: 2001-12-06

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0
 Description (
human factor
 Sequence
 93.48;
ilarity 96.08;
Conservative
 SEQ ID NO 1
LENGTH: 1438
TYPE: PRT
ORGANISM: Artificial S
FEATURE:
) OTHER INFORMATION:
; OTHER INFORMATION:
US-10-006-091-1
 Query Match
Best Local S
Matches 24
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Gaps ö Indels 508  $\Box$  $\sim$ ò: RPNYSRRLPKGVKHLKDFPILPGEI 1 Similarity 24; Conserv 484 QQ õ

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RESULT 2
US-10-047-257-1
Sequence 1, Application US/10047257
Patent No. US20020115152A1
GENERAL INFORMATION:
APPLICANT: Cho, Myung-Sam
APPLICANT: Chan, Sham-Yuen
APPLICANT: Kelsey, William
APPLICANT: Yee, Helena

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LENGTH: 14
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 ORGANISM:
S-10-095-718
 SOFTWARE:
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 Sequence:
TITLE OF INVENTION: Expression System for Factor VIII FILE REFERENCE: MSB-7255.2 CURRENT APPLICATION NUMBER: US/10/047,257 CURRENT FILING DATE: 2002-01-15 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.0
 VIII
 Score 127; DB 12
Pred. No. 2.8e-11
; Mismatches
 factor
 Same
 RESULT 3
US-10-095-718-2
Sequence 2, Application US/10095718
Patent No. US20020131956A1
GENERAL INFORMATION:
APPLICANT: Walsh, Christopher
APPLICANT: Burstein, Haim
APPLICANT: Lynch, Carmel
APPLICANT: Lynch, Carmel
APPLICANT: Stepan, Tony
APPLICANT: Munson, Keith
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 35052/204375
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
 sedneuce
 Score 127; DB
Pred. No. 2.8e-
0; Mismatches
 of Artificial . VIII sequence
 Sequence 2, Application US/09957641; Publication No. US20020182670A1; Publication No. US20020182670A1; GENERAL INFORMATION:
TITLE OF INVENTION: MODIFIED FACTOR VIII; FILE REFERENCE: 75-00; CURRENT APPLICATION NUMBER: US/09/957,641; CURRENT FILING DATE: 2001-09-16
 BDD FVIII
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 Description of human factor
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 Sequence
 93.4%;
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 ORGANISM: Artificial
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 INFORMATION:
 ORGANISM: HOMO
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US-09-957-641-2
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 FEATURE:
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 Length 2332;
 Length 1431
 Indels
 Score 101; DB 12;
Pred. No. 2.6e-07;
;; Mismatches 3
 Score 127; DB 9;
Pred, No. 4.8e-11
; Mismatches
 VII
 APPLICANT: Lynch, Carmel
APPLICANT: Stepan, Tony
APPLICANT: Stepan, Tony
APPLICANT: Munson, Keith
TITLE OF INVENTION: Methods of Using the Sam
FILE REFERENCE: 35052/204375
CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 5
 factor
 4
 60/234047
 60/236460
 Sequence 4, Application US/10095718

Sequence 4, Application US/10095718

Patent No. US20020131956A1

GENERAL INFORMATION:

APPLICANT: Walsh, Christopher

APPLICANT: Chao, Hengjun

APPLICANT: Lynch, Carmel

APPLICANT: Lynch, Carmel

APPLICANT: Stepan, Tony

APPLICANT: Stepan, Tony

TITLE OF INVENTION:

TITLE OF INVENTION:
 Version
 Sequence 49, Application US/09949192;
Patent No. US20020142292A1
GENERAL INFORMATION:
APPLICANT: Parham, Christi L.
APPLICANT: Gorman, Daniel L.
APPLICANT: Kurata, Hirokazu
APPLICANT: Arai, Naoko
APPLICANT: Arai, Naoko
APPLICANT: Sana, Theodore R.
APPLICANT: Sana, Theodore B.
APPLICANT: Savkoor, Chetan
APPLICANT: Savkoor, Chetan
APPLICANT: Savkoor, Chetan
APPLICANT: Savkoor, Chetan
APPLICANT: Smith, Kathleen M.
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 RPNYSRRLPKGVKHLKDFPILPGE1
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 PNYSRRLPKGVKHLKDFPILPGEI
PRIOR APPLICATION NUMBER: US 60 PRIOR FILING DATE: 2000-09-19 PRIOR APPLICATION NUMBER: US 60 PRIOR FILING DATE: 2000-09-29 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0
 74.3%;
ilarity 79.2%;
Conservative
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 93.48;
96.08;
 Conservative
 ORGANISM: Homo sapiens
S-09-957-641-2
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19; Conser
 SEQ ID N
FastSEQ
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 RESULT 6
US-09-949-192-49
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 US-09-733-524-7

Sequence 7, Application US/09733524

Sequence 7, Application US/09733524

GENERAL INFORMATION:

APPLICANT: The Governers of the University of Alberta, a Ca APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

APPLICANT: Taylor, Diane E.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3

TITLE OF INVENTION: FUGCOSYLTRANSFERASES AND EXPRESSION SYS:

TITLE OF INVENTION: EXPRESSING THEM

FILE REFERENCE: 07254/649002

CURRENT FILING DATE: 2000-12-14

PRIOR FILING DATE: 1997-06-06

SOFTWARE: FastSFO C

SOFTWARE: FastSFO C

SEQ ID NO C
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 A APPLICATION NUMBER: 18 DATE: 1998-06-05
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 Score 48.5; DB Pred. No. 7.1; 3; Mismatches
 Pred. No. 6.6; ; Mismatches
 ed. No. 7.1;
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 RESULT 9
US-10-120-319-11
Sequence 11, Application US/10120319
Patent No. US20020164749A1
GENERAL INFORMATION:
APPLICANT: Taylor, Diane E.
APPLICANT: Ge, Zhongming
TITLE OF INVENTION: ALPHA-1, 3-FUCOS;
FILE REFERENCE: 07254/049001
CURRENT APPLICATION NUMBER: US/10/12(CURRENT FILING DATE: 2002-04-09)
PRIOR FILING DATE: EARLIER FILING DATE;
PRIOR APPLICATION NUMBER: EARLIER FILING DATE;
PRIOR FILING DATE: FASTESQUE FOR WINDER FILING DATE;
PRIOR FILING DATE: FASTESQUE FILING FILING PATE;
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 TYPE: PRT
ORGANISM: Mus musculus
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LENGTH: 433
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 METHODS AND PRODUCTS FOR THE SYNTHESIS
OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,
GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION
OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTURES:
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LATION INFORMATION:

LELEPHONE: (703)521-4500

TELEFAX: (703)486-2347

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 Jefferson Davis
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 4
 Floppy disk
M PC compatible
STEM: PC-DOS/MS-
 FILING DATE: 24-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/914,2
FILING DATE: 20-JUL-1992
ATTORNEY/AGENT INFORMATION:
 NT APPLICATION DATA:
APPLICATION NUMBER: US/09/8
FILING DATE: 24-May-2001
 4
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MSSOFTWARE: Patentin Release
 CURRENT APPLICATION NUMBER: US/09/949
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/231,267
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
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 -KGLEHKADLOOHLFPVPPGHL
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 SPIVAK,
 CANT: McClanahan, Terrill K.
OF INVENTION: MAMMALIAN GENES
REFERENCE: DX01169K
 Sequence 8, Application US/0986347
Patent No. US20020102688A1
GENERAL INFORMATION:
APPLICANT: LOWE, JOHN B.
TITLE OF INVENTION: METHODS
 Ŋ
 SEQ
 FORM:
 .78;
 OLOGY: unknown
TYPE: protein
DESCRIPTION: S
 OBLON,
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CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
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 INFORMATION FOR SEQUENCE C
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 APPLICANT: Farwick, Mike
APPLICANT: Farwick, Mike
APPLICANT: Huthmacher, Klaus
APPLICANT: Huthmacher, Raus
APPLICANT: Huthmacher, Raus
APPLICANT: Pfefferle, Walter
TITLE OF INVENTION: New Nucleotide Sequences Which Code for the menE
FILE REFERENCE: 21123/280112
CURRENT APPLICATION NUMBER: US/09/834,722
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
 ij
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 376;
 Length 345;
 Length
 Indels
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 ore 47; DB 9 ed. No. 9.2; Mismatches
 Score 44.5;
Pred. No. 25;
 APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PFLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 6584
LENGTH: 345
 Mismatche
 Score 47;
Pred. No.
 -09-738-626-6584
Sequence 6584, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
 Corynebacterium glutamicum -6584
 Corynebacterium glutamicum -2
 RESULT 11
US-09-834-722-2
; Sequence 2, Application US/09834722
; Patent No. US20020102663A1
; GENERAL INFORMATION:
 366
 4
 19
 32.7%;
ilarity 52.6%;
Conservative
 34.6%;
50.0%;
 155
 NAKAGAWA, SATOSHI
MIZOGUCHI, HIROSI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
 RANYEREVPRGAFIHVDDFP
RPNYSRRLPKGV-KHLKDFP
 Similarity 50. 9; Conservative
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 TYPE: PRT
ORGANISM:
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 TYPE:
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 APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: TKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
 NW.
 BER: US/09/893
-Jun-2001
 COUNTRY: USA
ZIP: 20005-3934

ZIP: 20005-3934

PUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-ISOFTWARE: Patentin Release #
 KESSLER,
ORK AVE.,
 00/280988
 Sequence 4005, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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 RESULT 13
US-09-893-637-2
; Sequence 2, Application US/09893637
; Patent No. US20020049313A1
; GENERAL INFORMATION:
 SUSANNA
Method f
Higher E
 CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KES
STREET: 1100 NEW YORK
CITY: WASHINGTON
 MATTHEW
 NAKAGAWA, SATOSHI
MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
 CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-Jun-
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 N NUMBER: JP 0
E: 2000-08-03
NOS: 7059
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 32.78;
 ADAM
 ORGANISM: Corynebacterium -09-738-626-4005
 RLPKGVKHLKDFP-ILPGE
RLPKGVKHLKDFP-1LPGE
 OLPKRIKHLESLPSIGPGK
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OLPKRLKHLESLPSIGPGK
 T: COTTEN, M
BAKER, AD
CHIOCCA,
INVENTION:
 SEQUENCES:
 F SEQ ID NOS: 70: Patentin ver. 4005
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 DATE:
 APPLICATION
FILING DATE:
 CITY: V
 APPLICANT:
 OF.
 RESULT 12
US-09-738-626-4005
 OF
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 37391..38239 /note=ORF8
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 APPLICATION NUMBER: US 08/750,180
FILING DATE: 14-FEB-1997
APPLICATION NUMBER: PCT/EP95/01989
FILING DATE: 26-MAY-1995
APPLICATION NUMBER: DE P 44 18 825.0
FILING DATE: 30-MAY-1994
APPLICATION NUMBER: DE P 44 42 587.2
FILING DATE: 30-NOY-1994
ATTORNEY/AGENT INFORMATION:
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ed. No. 21;
Mismatches
 Score 44; DB Pred. No. 21; 2; Mismatches
 ΩB
 Sequence 21, Application US/09970711

Patent No. US20020081279A1

GENERAL INFORMATION:

APPLICANT: Baker, Adam

APPLICANT: Cotten, Matthew

APPLICANT: Chiocca, Susanna

APPLICANT: Kurzbauer, Robert

APPLICANT: Schaffner, Gotthold

TITLE OF INVENTION: Chicken Embryo Lethal

FILE REFERENCE: 0652.1800001

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/171,461

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1997-04-18
 NAME: Peter A. Jackman
REGISTRATION NUMBER: 45,986
REFERENCE/DOCKET NUMBER: 0652.18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
 Embryo Lethal
 Score 44;
Pred. No.
 ID NO:
 <Unknown>
 T 14
-970-711-21
puence 21, Application US/09970711
ent No. US20020081279A1
 5
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 ;
TYPE: amino acid
;
TOPOLOGY: linear
;
MOLECULE TYPE: Protein
;
SEQUENCE DESCRIPTION: SEC
 142
 APPLICATION DATA:
 32.4%;
52.6%;
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 14
 th 32.4%;
Similarity 52.6%;
10; Conservative
 Position:
 YSRRLPKGVKHLKD - - FPI
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 YSRRLPKGVKHLKD--FPI
 CLASSIFICATION:
APPLICATION DA
 54
 SEQ 1D NOS: 5 PatentIn Ver.
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10; Conserv
 THER INFORMATION: -970-711-21
 NO 21
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 ORGANISM:
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 Length
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39;
 Score 44; DB
Pred. No. 39;
4; Mismatches
 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Holtzmann, Douglas

TITLE OF INVENTION: NOVEL GENES ENCODING PR

FILE REFERENCE: 7853-226-999

CURRENT APPLICATION NUMBER: US/09/796,858

CURRENT FILING DATE: 2001-03-01

PRIOR FILING DATE: 1998-12-30

 09:05:29
 APPLICATION NUMBER: 09/572,002
APPLICATION NUMBER: 09/572,002
FILING DATE: 2000-05-14
APPLICATION NUMBER: 09/597,993
APPLICATION NUMBER: 09/597,993
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 474,071
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 336,536
 09/471,179
 365,164
 09/630,334
 09/312,359
 342,687
e 40, Application US/09796858
No. US20020055139A1
, INFORMATION:
 7665/
 79097
 399,
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7
 2003,
 R APPLICATION NUMBER: 09/31
R FILING DATE: 1999-05-14
R APPLICATION NUMBER: 09/33
R FILING DATE: 1999-06-18
R APPLICATION NUMBER: 09/34
R FILING DATE: 1999-06-29
R FILING DATE: 1999-09-20
R APPLICATION NUMBER: 09/47
R FILING DATE: 1999-12-23
R FILING DATE: 1999-12-23
R FILING DATE: 1999-12-23
R APPLICATION NUMBER: 09/47
R FILING DATE: 1999-12-29
R APPLICATION NUMBER: 09/47
 R FILING DATE: 2000-06-12
R APPLICATION NUMBER: 09/59
R FILING DATE: 2000-06-22
R APPLICATION NUMBER: 09/60
R FILING DATE: 2000-06-29
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 APPLICATION NUMBER: 09/
FILING DATE: 2000-09-20
R OF SEQ ID NOS: 50
 60
 A APPLICATION NUMBER: US, R FILING DATE: 1999-07-3(R APPLICATION NUMBER: 09, NOTE: 2000-07-3)
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